RAW SEQUENCE LISTING

EF-S

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Application Serial Number: _10/796,669B_
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Date Processed by STIC: _4/10/07_

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RAW SEQUENCE LISTING   DATE: 04/10/2007
PATENT APPLICATION: US/10/796,669B   TIME: 17:35:16

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 3 <110> APPLICANT: Wang, Jin-Town
 4        Lin, Tzu-Lung
 6 <120> TITLE OF INVENTION: A TYPE II RESTRICTION ENDONUCLEASE AND APPLICATION THEREOF
 8 <130> FILE REFERENCE: P/741-179
10 <140> CURRENT APPLICATION NUMBER: 10/796,669B
11 <141> CURRENT FILING DATE: 2004-03-09
13 <160> NUMBER OF SEQ ID NOS: 15
15 <170> SOFTWARE: PatentIn version 3.3
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18 <211> LENGTH: 5
19 <212> TYPE: DNA
20 <213> ORGANISM: Helicobacter pylori
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28 <212> TYPE: DNA
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41 cga aac cct aaa aga ata gga caa ttt tta gct gtt tta gga aag ttt      96
42 Arg Asn Pro Lys Arg Ile Gly Gln Phe Leu Ala Val Leu Gly Lys Phe
43              20                  25                  30
45 gaa aat caa atc ctt aaa tct tca ata atc atg caa att atc aaa tcc     144
46 Glu Asn Gln Ile Leu Lys Ser Ser Ile Ile Met Gln Ile Ile Lys Ser
47          35                  40                  45
49 gtt ttg gct cat agg ctt tat aga cct act tct ctc aat caa aat aaa     192
50 Val Leu Ala His Arg Leu Tyr Arg Pro Thr Ser Leu Asn Gln Asn Lys
51      50                  55                  60
53 gaa ttg aaa gaa aaa ttt gac tcc aat gaa tat gtc ttt agc gat gaa     240
54 Glu Leu Lys Glu Lys Phe Asp Ser Asn Glu Tyr Val Phe Ser Asp Glu
55 65                  70                  75                  80
57 gag tta gaa cgc att ata gaa ata tcc cca caa aat cat aaa gaa atg     288
58 Glu Leu Glu Arg Ile Ile Glu Ile Ser Pro Gln Asn His Lys Glu Met
59                  85                  90                  95
61 ggc ttt gag cat gga tgg gaa agc cgg ttt gac act tgg tat aag ctt     336
62 Gly Phe Glu His Gly Trp Glu Ser Arg Phe Asp Thr Trp Tyr Lys Leu
63              100                 105                 110
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65 atg tgt gag ttt ggt ttt tgc tac tat gca aaa tat gag aaa ata ctc       384
66 Met Cys Glu Phe Gly Phe Cys Tyr Tyr Ala Lys Tyr Glu Lys Ile Leu
67         115                 120                 125
69 atc agc gat agc gct aag atg ctt att ctt gct tat tac aat aaa gaa       432
70 Ile Ser Asp Ser Ala Lys Met Leu Ile Leu Ala Tyr Tyr Asn Lys Glu
71         130                 135                 140
73 aac gat gct ttt aaa gaa agc gtt gat gaa agc gta gtt ggg gct ata       480
74 Asn Asp Ala Phe Lys Glu Ser Val Asp Glu Ser Val Val Gly Ala Ile
75 145                 150                 155                 160
77 ttt tta aac gct ctg tct aaa tat gaa gta gga aac cct tac aaa aag       528
78 Phe Leu Asn Ala Leu Ser Lys Tyr Glu Val Gly Asn Pro Tyr Lys Lys
79                 165                 170                 175
81 aat tta aac cat aac aac cct ttc aaa cta ttg ctc tcg ctt tta aaa       576
82 Asn Leu Asn His Asn Asn Pro Phe Lys Leu Leu Leu Ser Leu Leu Lys
83             180                 185                 190
85 cga ctc aaa aat gcc cat cta acc ccc cta tct gtc aaa gaa atc cct       624
86 Arg Leu Lys Asn Ala His Leu Thr Pro Leu Ser Val Lys Glu Ile Pro
87         195                 200                 205
89 att tta ctt tgt tgg aaa gac gat aac gct aat ggg ctt tat gac tac       672
90 Ile Leu Leu Cys Trp Lys Asp Asp Asn Ala Asn Gly Leu Tyr Asp Tyr
91         210                 215                 220
93 att att cgt tta aga caa gaa atc gtt act atc aat aaa aca gaa ttc       720
94 Ile Ile Arg Leu Arg Gln Glu Ile Val Thr Ile Asn Lys Thr Glu Phe
95 225                 230                 235                 240
97 agc tac tca gat gaa ttt atc tat gaa aaa tgc cta aaa ctt tta gaa       768
98 Ser Tyr Ser Asp Glu Phe Ile Tyr Glu Lys Cys Leu Lys Leu Leu Glu
99                 245                 250                 255
101 agt gtt aat aaa aca cga ttt aaa atg agc caa atc act aac gaa gcc      816
102 Ser Val Asn Lys Thr Arg Phe Lys Met Ser Gln Ile Thr Asn Glu Ala
103                 260                 265                 270
105 gtt gat gaa tac att aga aaa atg cgt att aca gga ctt att tca ttg      864
106 Val Asp Glu Tyr Ile Arg Lys Met Arg Ile Thr Gly Leu Ile Ser Leu
107         275                 280                 285
109 cgt ggt aat ggt agg ttt att gat att aat act aat gaa aat aat aaa      912
110 Arg Gly Asn Gly Arg Phe Ile Asp Ile Asn Thr Asn Glu Asn Asn Lys
111         290                 295                 300
113 ata gat tac att tta caa acc cat aag gct ttt aaa ggg gat tat tta      960
114 Ile Asp Tyr Ile Leu Gln Thr His Lys Ala Phe Lys Gly Asp Tyr Leu
115 305                 310                 315                 320
117 aac gac act caa gct aac aaa ctc gcc ttt ttt aac tac atg gcg atc      1008
118 Asn Asp Thr Gln Ala Asn Lys Leu Ala Phe Phe Asn Tyr Met Ala Ile
119                 325                 330                 335
121 gtg gat agc ttt ctt gtt agt gtt act cca atc agc gct aat gag agc      1056
122 Val Asp Ser Phe Leu Val Ser Val Thr Pro Ile Ser Ala Asn Glu Ser
123             340                 345                 350
125 gtt aaa tca agc aaa ttg aat gaa cta gca aac act tat act aaa gat      1104
126 Val Lys Ser Ser Lys Leu Asn Glu Leu Ala Asn Thr Tyr Thr Lys Asp
127         355                 360                 365
129 ttt atc aag caa gaa tta ctc att act tgt aac aag caa gaa tca aaa      1152
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130 Phe Ile Lys Gln Glu Leu Leu Ile Thr Cys Asn Lys Gln Glu Ser Lys
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133 gat agt ttt tta aga ctc att gat aaa cct tta cgc tta gaa ttt tta      1200
134 Asp Ser Phe Leu Arg Leu Ile Asp Lys Pro Leu Arg Leu Glu Phe Leu
135 385                 390                 395                 400
137 agc gct att ttc ttg aaa caa cat ttt gaa aat tta agc gtg ata ccc      1248
138 Ser Ala Ile Phe Leu Lys Gln His Phe Glu Asn Leu Ser Val Ile Pro
139             405                 410                 415
141 aat tat aaa agc gat gat gaa ggc ttg ccc gta tac aca gca agc ggt      1296
142 Asn Tyr Lys Ser Asp Asp Glu Gly Leu Pro Val Tyr Thr Ala Ser Gly
143             420                 425                 430
145 aat aaa cct gat att gta gct atg gac aca aaa gcc caa agt tat ata      1344
146 Asn Lys Pro Asp Ile Val Ala Met Asp Thr Lys Ala Gln Ser Tyr Ile
147         435                 440                 445
149 gaa gtg agc ttg att aga gac aga agt caa agt acc ttg gaa atg ata      1392
150 Glu Val Ser Leu Ile Arg Asp Arg Ser Gln Ser Thr Leu Glu Met Ile
151     450                 455                 460
153 cct att gcc aga cat tta aaa gaa ttg att aaa aat agc acc gat att      1440
154 Pro Ile Ala Arg His Leu Lys Glu Leu Ile Lys Asn Ser Thr Asp Ile
155 465                 470                 475                 480
157 aga gaa aaa ttt agt gtt ttt gta gct cca aat atc cat gat gat gcc      1488
158 Arg Glu Lys Phe Ser Val Phe Val Ala Pro Asn Ile His Asp Asp Ala
159             485                 490                 495
161 aaa gaa tat gcg gaa ttt gcc caa ttc aaa gac aat att aat ata tgt      1536
162 Lys Glu Tyr Ala Glu Phe Ala Gln Phe Lys Asp Asn Ile Asn Ile Cys
163             500                 505                 510
165 tgt tat gct att aat gat ttt atc aaa aaa gta gaa aac agc ata gaa      1584
166 Cys Tyr Ala Ile Asn Asp Phe Ile Lys Lys Val Glu Asn Ser Ile Glu
167         515                 520                 525
169 tgg tta cag atc aat gac cat ttg aaa gct taa                          1617
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186             20                  25                  30
189 Glu Asn Gln Ile Leu Lys Ser Ser Ile Ile Met Gln Ile Ile Lys Ser
190         35                  40                  45
193 Val Leu Ala His Arg Leu Tyr Arg Pro Thr Ser Leu Asn Gln Asn Lys
194     50                  55                  60
197 Glu Leu Lys Glu Lys Phe Asp Ser Asn Glu Tyr Val Phe Ser Asp Glu
198 65                  70                  75                  80
201 Glu Leu Glu Arg Ile Ile Glu Ile Ser Pro Gln Asn His Lys Glu Met
202             85                  90                  95
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205 Gly Phe Glu His Gly Trp Glu Ser Arg Phe Asp Thr Trp Tyr Lys Leu
206          100               105              110
209 Met Cys Glu Phe Gly Phe Cys Tyr Tyr Ala Lys Tyr Glu Lys Ile Leu
210      115               120              125
213 Ile Ser Asp Ser Ala Lys Met Leu Ile Leu Ala Tyr Tyr Asn Lys Glu
214      130               135              140
217 Asn Asp Ala Phe Lys Glu Ser Val Asp Glu Ser Val Val Gly Ala Ile
218 145               150               155              160
221 Phe Leu Asn Ala Leu Ser Lys Tyr Glu Val Gly Asn Pro Tyr Lys Lys
222               165               170              175
225 Asn Leu Asn His Asn Asn Pro Phe Lys Leu Leu Leu Ser Leu Leu Lys
226           180               185              190
229 Arg Leu Lys Asn Ala His Leu Thr Pro Leu Ser Val Lys Glu Ile Pro
230          195               200              205
233 Ile Leu Leu Cys Trp Lys Asp Asp Asn Ala Asn Gly Leu Tyr Asp Tyr
234      210               215               220
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238 225               230               235              240
241 Ser Tyr Ser Asp Glu Phe Ile Tyr Glu Lys Cys Leu Lys Leu Leu Glu
242               245               250              255
245 Ser Val Asn Lys Thr Arg Phe Lys Met Ser Gln Ile Thr Asn Glu Ala
246           260               265              270
249 Val Asp Glu Tyr Ile Arg Lys Met Arg Ile Thr Gly Leu Ile Ser Leu
250      275               280              285
253 Arg Gly Asn Gly Arg Phe Ile Asp Ile Asn Thr Asn Glu Asn Asn Lys
254      290               295               300
257 Ile Asp Tyr Ile Leu Gln Thr His Lys Ala Phe Lys Gly Asp Tyr Leu
258 305               310               315              320
261 Asn Asp Thr Gln Ala Asn Lys Leu Ala Phe Phe Asn Tyr Met Ala Ile
262           325               330              335
265 Val Asp Ser Phe Leu Val Ser Val Thr Pro Ile Ser Ala Asn Glu Ser
266           340               345              350
269 Val Lys Ser Ser Lys Leu Asn Glu Leu Ala Asn Thr Tyr Thr Lys Asp
270           355               360              365
273 Phe Ile Lys Gln Glu Leu Leu Ile Thr Cys Asn Lys Gln Glu Ser Lys
274      370               375              380
277 Asp Ser Phe Leu Arg Leu Ile Asp Lys Pro Leu Arg Leu Glu Phe Leu
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281 Ser Ala Ile Phe Leu Lys Gln His Phe Glu Asn Leu Ser Val Ile Pro
282           405               410              415
285 Asn Tyr Lys Ser Asp Asp Glu Gly Leu Pro Val Tyr Thr Ala Ser Gly
286           420               425              430
289 Asn Lys Pro Asp Ile Val Ala Met Asp Thr Lys Ala Gln Ser Tyr Ile
290           435               440              445
293 Glu Val Ser Leu Ile Arg Asp Arg Ser Gln Ser Thr Leu Glu Met Ile
294      450               455              460
297 Pro Ile Ala Arg His Leu Lys Glu Leu Ile Lys Asn Ser Thr Asp Ile
298 465               470               475              480
301 Arg Glu Lys Phe Ser Val Phe Val Ala Pro Asn Ile His Asp Asp Ala
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302                    485                490                495
305 Lys Glu Tyr Ala Glu Phe Ala Gln Phe Lys Asp Asn Ile Asn Ile Cys
306             500                505                510
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314      530                535
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330 1               5                  10                 15
332 ttt aat caa gct tta aag cta gaa gaa aat tat ttt agc caa cat ttt     96
333 Phe Asn Gln Ala Leu Lys Leu Glu Glu Asn Tyr Phe Ser Gln His Phe
334             20                 25                 30
336 agc aac aag ttt ttc agc tat aaa gat tgt gtc aaa atc ggt agc att    144
337 Ser Asn Lys Phe Phe Ser Tyr Lys Asp Cys Val Lys Ile Gly Ser Ile
338             35                 40                 45
340 aga gag cat ata gaa agc tta aac tta gat aaa tta aat aaa gat att    192
341 Arg Glu His Ile Glu Ser Leu Asn Leu Asp Lys Leu Asn Lys Asp Ile
342      50                 55                 60
344 tta tta aca agc ctg att tat tca atg gat aag ata gct aac acg gta    240
345 Leu Leu Thr Ser Leu Ile Tyr Ser Met Asp Lys Ile Ala Asn Thr Val
346 65                 70                 75                 80
348 ggg cat tat gaa gct tat agg aaa aaa gag att ttg caa gat aga ttt    288
349 Gly His Tyr Glu Ala Tyr Arg Lys Lys Glu Ile Leu Gln Asp Arg Phe
350             85                 90                 95
352 att ttt gag ctt att agc cct ata aaa cat gat aaa aat atc atg ata    336
353 Ile Phe Glu Leu Ile Ser Pro Ile Lys His Asp Lys Asn Ile Met Ile
354             100                105                110
356 gag aga aaa aac gct aac gaa ttg gct aaa acc tta aaa ata gac tta    384
357 Glu Arg Lys Asn Ala Asn Glu Leu Ala Lys Thr Leu Lys Ile Asp Leu
358             115                120                125
360 gtc ttt att gat cct cca tac aat tca agg caa tac agc cgg ttt tat    432
361 Val Phe Ile Asp Pro Pro Tyr Asn Ser Arg Gln Tyr Ser Arg Phe Tyr
362      130                135                140
364 cat ctc tat gaa aac cta gtg cag tgg aaa aaa ccc aaa ctc tat gga    480
365 His Leu Tyr Glu Asn Leu Val Gln Trp Lys Lys Pro Lys Leu Tyr Gly
366 145                150                155                160
368 aca gct tta aag cca tca tgc gag aac atg agc gaa tat tgc cgc tct    528
369 Thr Ala Leu Lys Pro Ser Cys Glu Asn Met Ser Glu Tyr Cys Arg Ser
370             165                170                175
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VERIFICATION SUMMARY   DATE: 04/10/2007
PATENT APPLICATION: **US/10/796,669B** TIME: 17:35:17

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